

GCCAGCTTCTACGCTGCCTTCAGGACACAGACGTGCCCAATCATGGCTTCTTGGTGCTTGATTACAGCTCAAGTCTGGG
 TCAAAATGAAGGGAGATGTGGTGGGCAGCCGAGCCCTCAGCAACACAAGCGGAGCACAGGAACACCTCAGGGTCTTCC
 AGTTCCTCATCTCAGAAGGCTCAATGAAATCCTTCTTCTGTCCACACCATCGTGCTTATCAGGGAGAATGTGTGCAAG
 TGTGGCTATGCCAGAGCCAGCACATGGGAAGGCCACCCAGATCAACCAAAGTGAGAAATGGAATCACAAGAAACACACCA
 AGGAATTTCTACCGACGCCCTTGGGGATATTAGTTTGAGACACTGGGGAAGAAAGGGAAGTATATACGTCTGTCTTG
 CGACACGGACGCCGAAATCCTTACGAGCTGCTGACCCAGCACTGGCACCTGAAAACACCAACCTGGTCATTTCTGTG
 ACCGGGGGCGCCAAAGAACTTCGCCCTGAAGCCGCGCATGCGCAAGATCTTCAGCCGGCTCATCTACATCGCGCAGTCCA
 AAGGTGCTTGGATTCTCACGGGAGGCACCCATTATGGCTGATGAAGTACATCGGGGAGGTGGTGAGAGATAACACCAT
 CAGCAGGAGTTTCAGAGGAGAATATTGTGGCCATTGGCATAGCAGCTTGGGGCATGGTCTCCAACCGGGACACCCCTCATC
 AGGAATTGCGATGCTGAGGGCTATTTTTTAGCCAGTACCTTATGGATGACTTCACAAGAGATCCACTGTATATCCTGG
 ACAACAACCACACACATTTGCTGCTCGTGGACAATGGCTGTCTGACATCCCACTGTGCAAGCAAAGCTCCGGAATCA
 GCTAGAGAAGTATATCTCTGAGCGCACTATTCAAGATTCCAACATATGGTGGCAAGATCCCCATTGTGTGTTTTGCCCAA
 GGAGGTGGAAAAGAGACTTTGAAAGCCATCAATACCTCCATCAAAAATAAAATTCCTTGTGTGGTGGTGGAAAGGCTCGG
 GCCAGATCGCTGATGTGATCGCTAGCCTGGTGGAGGTGGAGGATGCCCTGACATCTTCTGCCGTCAAGGAGAAGCTGGT
 GCGCTTTTTACCCCGCAGGCTGTCCCGGCTGCCTGAGGAGGAGACTGAGAGTTGGATCAAATGGCTCAAAGAAATTTCTC
 GAATGTTCTCACCTATTAACAGTTATTAATAATGGAAGAAGCTGGGGATGAAATTTGTGAGCAATGCCATCTCCTACGCTC
 TATACAAAGCCTTCAGCACCAAGTGAAGACAAGGATAACTGGAATGGGCAGCTGAAGCTTCTGCTGGAGTGAACCA
 GCTGGACTTAGCCAATGATGAGATTTTACCAATGACCGCCGATGGGAGAAGAGCAAACCGAGGCTCAGAGACACAATA
 ATCCAGGTCACATGGCTGGAAAATGGTAGAATCAAGTTGAGAGCAAAGATGTGACTGACGGCAAAGCCTCTTCTCATA
 TGCTGGTGGTTCTCAAGTCTGCTGACCTTCAAGAAGTATGTTTACGGCTCTCATAAAGGACAGACCCAAGTTTGTCCG
 CCTCTTTCTGGAGAATGGCTTGAACCTACGGAAGTTTCTACCCATGATGTCTCTACTGAACCTTTCTCCAACCACTTC
 AGCAGCTTGTGTACCGGAATCTGCAGATCGCCAAGAAATTCCTATAATGATGCCCTCCTCACGTTTGTCTGGAAGCTGG
 TTGCGAACTTCCGAAGAGGCTTCCGGAAGGAAGACAGAAATGGCCGGGACGAGATGGACATAGAATCCACGACGTGTC
 TCTTATTACTCGGCACCCCTGCAAGCTCTCTCATCTGGGCCATTCTTCAGAATAAGAAGGAACTCTCCAAGTCAAT
 TGGGAGCAGACCCAGGGGCTGCACCTGCGCAGCCCTGGGAGCCAGCAAGCTTCTGAAGACTCTGGCCAAAGTGAAGAAGC
 ACATCAATGCTGCTGGGGAGTCCGAGGAGCTGGCTAATGAGTACGAGACCCGGGCTGTTGAGCTGTTCACTGAGTGTTA
 CAGCAGCGATGAAGACTTGGCAGAACAGCTGCTGGTCTATTCTGTGAAGCTTGGGGTGAAGCAACTGTCTGGAGCTG
 GCGGTGGAGGCCACAGACCAGCATTTCTATCGCCAGCCTGGGGTCCAGGAGGGGAGGGCTGTGCCCGTCCCATGCTTGC
 AAGGATGCTGACGATGCCCTTATCTCTGGTCCAGGAAGAACTGTGCAAGCACAAGAAGCTGCTTTGGTACTATG
 TGGCGTTCTTCACTCCCCCTTCGTGGTCTTCTCCTGGAATGTGGTCTTCTACATCGCCTTCTCCTGCTGTTTGCCTA
 CGTGCTGCTCATGGATTTCCATTGCGTGCCACACCCCCCGAGCTGGTCTGTACTCGCTGGTCTTTGTCTCTTCTGT
 GATGAAGTGAGACAGATGGAGCAGGGGGTGGCGCTCGTGAGGAGGCTCGGGCAGCACAGGAGCCCACTGAGGGGGTGG
 GAGGCTCAGGCATGGTGGGCTGCAGGTCCCGAGCCCTGCCCCACGGGAAGGCAGCTACGGCCCGCCCCGGTTCCCCGCTC
 ACGCCACTCTTCCACACTTCCCTGCAAGCTGAGGGTGCCAGCTCTGGCCTTGGCCAGCCAGAAAGGGGCTCCACAG
 TGCAGCGGTGGGCTGAAGGGCTCCTCAAGTGCCGCAAGTGGGAGCCAGGCAGAGGAGGTGCCGAGAGCAAGCGAGG
 GCTGTGAGGACTGCCAGCACGCTGTACCTCTCAGAAGCGTAAGGGACTGGCTGATGTCTTATCAGGACTGGGAACAA
 CTGGGACAGTGTCTGCCCCACAAGTGGGTGGTACGTAAATGGGGTGAATTATTTACTGACCTGTGGAATGTGATGGAC
 ACGCTGGGGCTTTTTTACTTCATAGCAGGAATTGTATTTGCGCTCCACTCTTCTAATAAAAGCTCTTTGTATTCTGGAC
 GAGTCATTTTCTGCTGGACTACATTATTTCACTCTAAGATTGATCCACATTTTACTGTAAGCAGAACTTAGGACC
 CAAGATTATAATGCTGACAGGATGACGAGCATTGAGATGAGTCTCATCTGGAAGCTCCATTCCAACACTGAGGTTCTTT
 GAGTTTGTGGTTTTAATCAAAGCATTTCTGGGACATCCAGTCTATCATGAAGTCTATCTGATCGATGTGTTCTTCTC
 TTCTGTTCTCTTTGCGGTGTGGATGGTGGCCTTTGCGTGGCCAGGCAAGGGATCCTTAGGCAGAATGAGCAGCGCTG
 GAGGTGGATATTCCGTTCCGTCATCTACGAGCCCTACCTGGCCATGTTCCGGCCAGGTGCCCAGTGACGTGGATGGTACC
 ACGTATGACTTTGCCCACTGCACCTTCACTGGGAATGAGTCCAAGCCACTGTGTGTGGAGCTGGATGAGCACAACCTGC
 CCCGTTCCCCGAGTGGATCACCATCCCCCTGGTGTGCATCTACATGTTATCCACCAACATCTGTGCTGGTCAACCTGCT
 GGTCCCATGTTTGGGTGTGTAGCCGGTGGGCTAGTTAGGTTCTTGACTTTGGGACAGAAAATAATTTGAAAGTGAAGT
 CAAAAGCAAAAGCAAGCAAGAGATTGACTGCAAGCCAAAGTACACTCTAGCAGCCGCTGGTTTCAGGAGATGGACCT
 CAGCTGTCACTGCATGTCTCCAGCCAGCTAGGTGTTTGGCAGGGACAGGACGCCAAGGGCACAAGATATCGCTGGAGAT
 GCACAAAGGGAAAATTGCAGAATTTCTCAGGGACAACACAGATGGCCACTGGTTGTCAAGGAGACTTTAAGAACCAT
 CTCAGATGGGGCGGCTACACGGTGGGCACCGTCCAGGAGAACAATGACCAGGTCTGGAAGTTCCAGAGGTACTTCTGG
 TGCAGGAGTACTGCAGCCGCTCAATATCCCCCTTCCCCCTTATCGTCTTCTGCTTACTTCTACATGGTGGTGAAGAAGTG
 CTTCAAGTGTGCTGCAAGGAGAAAAACATGGAGTCTTCTGTCTGCTCTGTGGAGGCAGGTGAAGATGCTTACAATTAT
 AGGGAACATAAGGAAGGCTCAAAGAGCTTTTTGGGAGCCAGTGTGCCTTGATGCTAGTCTTTGCTGCCACTCTGATTCT
 GTTGCCTGTTTTATTGGAGGGCATTGGAATGCGTGA

FIGURE 1

MASWCLITAQ VVVKMGDQV GSRSPQQHQR STGTPQGLPV PISEGSMKSF LPVHTIVLIR
 ENVCKCGYAQ SQHMEGTQIN QSEKWNKKH TKEFPTDAFG DIQFETLGKK GKYIRLSCDT
 DAEILYELLT QHWHLKTPNL VISVTGGAKN FALKPRMRKI FSRLIYIAQS KGAWILTGGT
 HYGLMKYIGE VVRDNTISRS SEENIVAIGI AAWGMVSNRD TLIRNCDAEG YFLAQYLMDD
 FTRDPLYILD NNHTHLLLV D NGCHGHPTVE AKLRNQLKY ISERTIQDSN YGGKIPIVCF
 AQGGGKETLK AINTSIKNI PCVVVEGSGQ IADVIASLVE VEDALTSSAV KEKLVRFPLR
 TVSRPPEET ESWIKWLKEI LECSHLLTVI KMEEAGDEIV SNAISYALYK AFSTSEQDKD
 NWNQQLKLLL EWNQLDLAND EIFTNDRRWE KSKPRLRDTI IQVTWLENGR IKVESKDVT
 GKASSHMLVV LKSADLQEV FALIKDRPK FVRLFLENGL NLRKFLTHDV LTELFSNHFS
 TLVYRNQIA KNSYNDALLT FVWKLVANFR RGFRKEDRNG RDEMDIELHD VSPITRHPLQ
 ALFIWAILQN KKELSKVIWE QTRGCTLAAL GASKLLKTLA KVKNDINAAG ESEELANEYE
 TRAVELFTEC YSSDEDLAEQ LLVYSCEAWG GSNCLELAVE ATDQHFAIQP GVQRGGLCP
 HACKDADDAL ISGRKKPVD KHKLLWYV AFFTSPFVVF SWNVVFYIAF LLLFAIVLLM
DFHVSVPHPPE LVLYSLVFVL FCDEVQMEQ GVALVEEARA AQEPTGVGG SGMVGCRRSRA
 LPHGKAATAR PGSRSRHSFH TSLQAEAGASS GLGQPRKGLP QCSGGLKGSS SAAKVGAQAE
 EVPRASEGCE DCQHAVTSQK RKGLADVLSR TGNNWDSVCP TSGWYVNGVN YFTDLWNVMD
TLGLFYFIAG IVFRLHSSNK SSLYSGRVIF CLDYIIFTLR LIHIFTVSRN LGPKIIMLQR
 MTSIEMSSSG SSIPTLRFFE FVVLQISISG TSSHHEVMLS DRCVLLPVPL CGVDGGLCVA
 RQGILRQNEQ RWRWIFRSVI YEPYLA MFGQ VPSDVGTTY DFAHCTFTGN ESKPLCVELD
 EHNLPFRFPEW ITIPLVCIYM LSTNILLVNL LVAMFGCVAG GLVQVLDFTG ENNLKVSQKQ
 KQARELTAKP KYTLAAAGFR RWTSAVTACL QPARCLPGTG RQGHKISLEM HKGKIAEFSQ
 GQHQMATGCQ GDFKNHLRWG GYTVGTQEN NDQVWKFQRY FLVQEYCSRL NIPFPFIVFA
YFYMVVKKCF KCCCKEKNME SSVCSVEAGE DAYNYREHKE GSKELFGSOC ALMLVFAATL
IRCLFYLEGI GNA

FIGURE 2

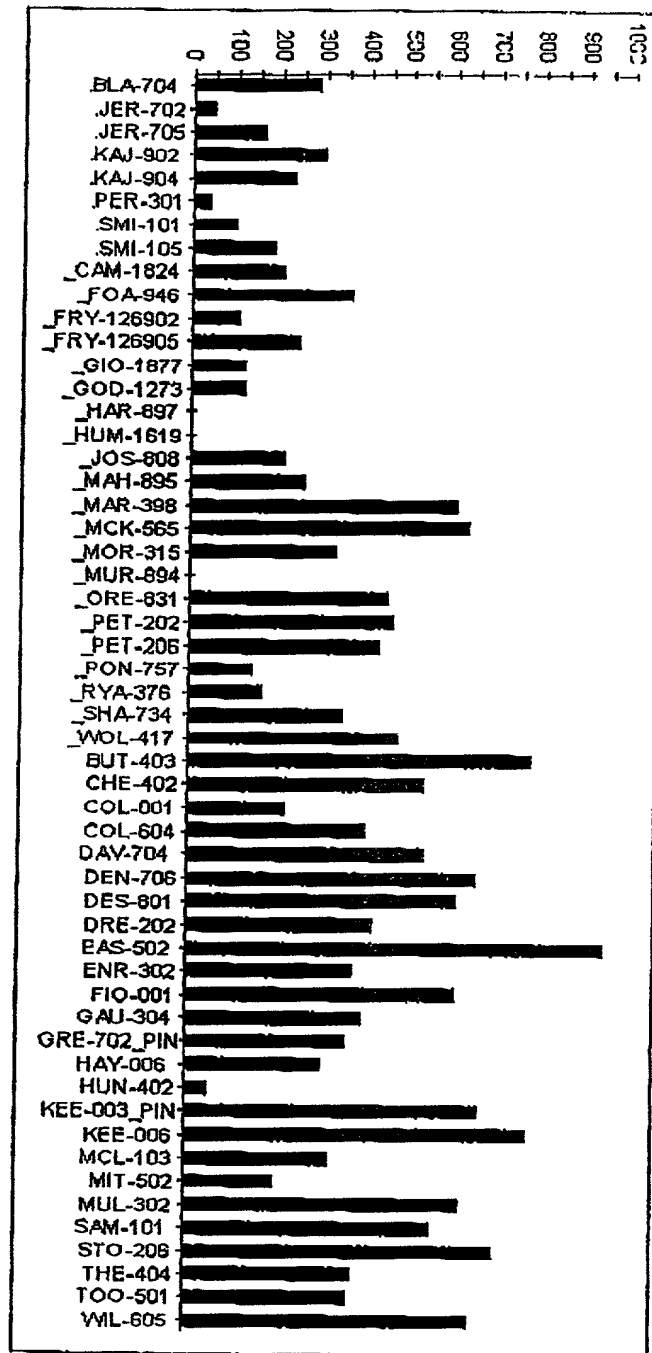


FIGURE 3A

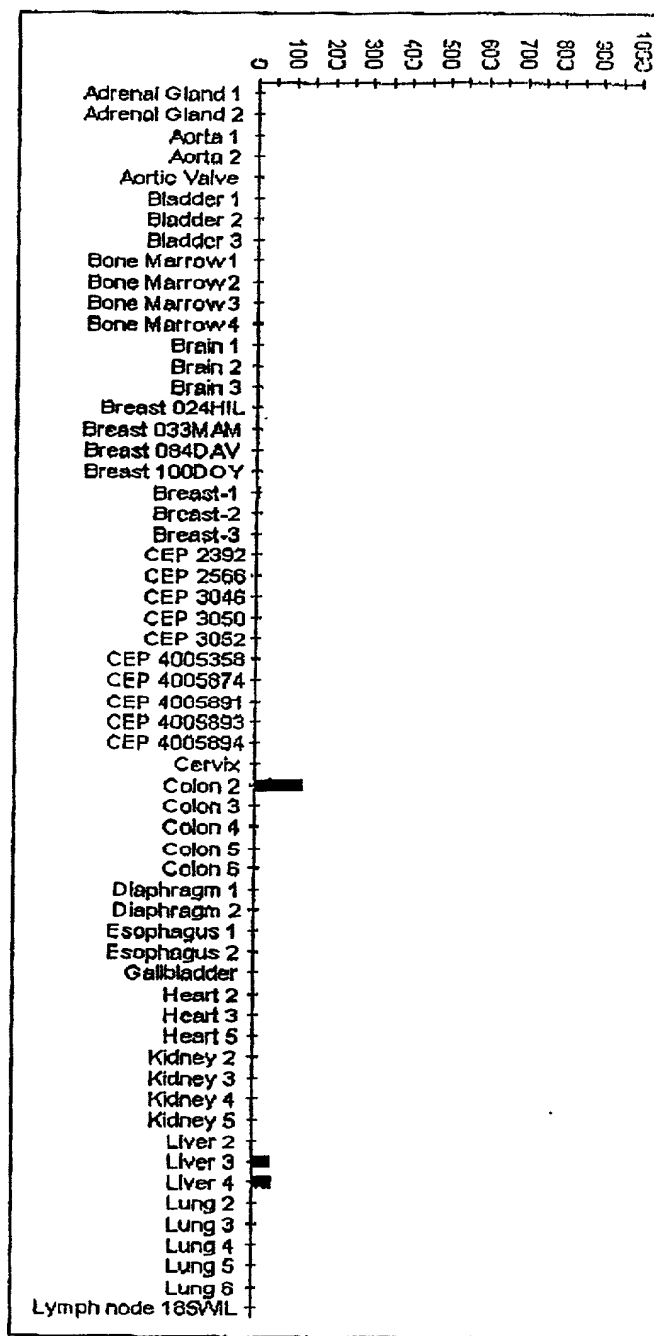


FIGURE 3B

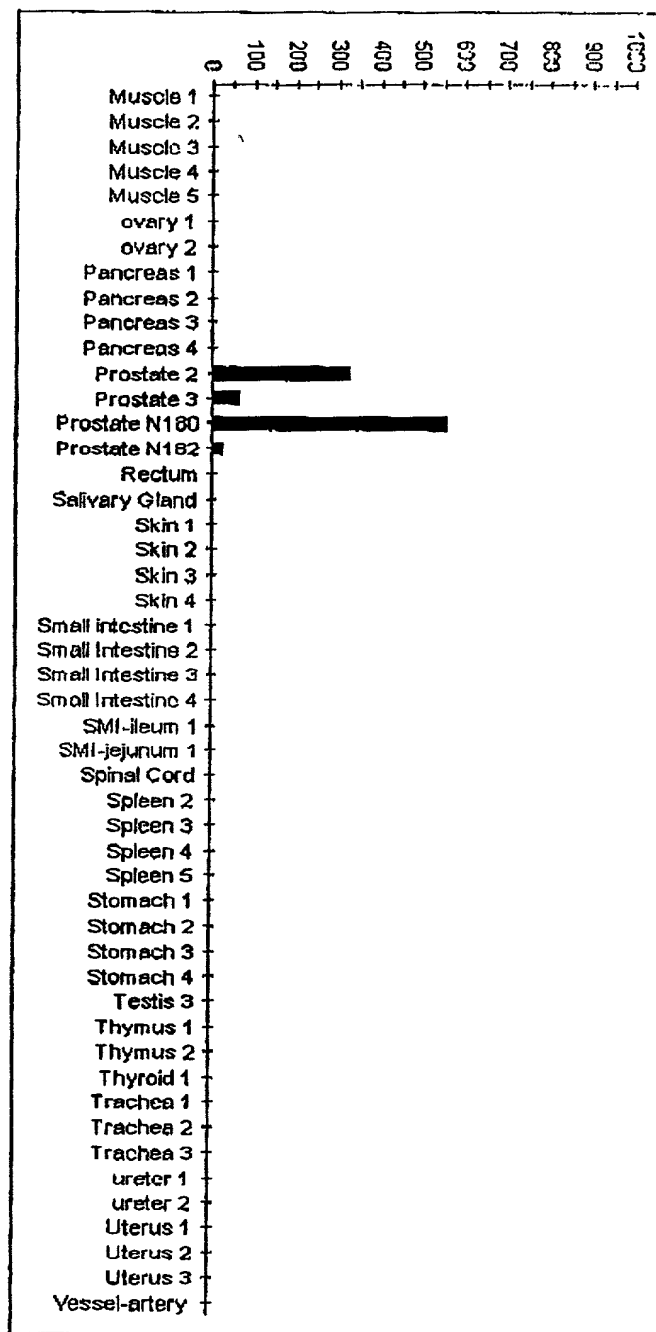


FIGURE 3C

Score = 457 bits (1162), Expect = e-127
Identities = 267/694 (38%), Positives = 385/694 (55%), Gaps = 88/694 (12%)

Query: 63 VCKCGYASQSRMEGT---QINQSEKWNYYKHTKEPPTDAFGDIQFETLGKK-GKYIRLSC 118
VC+COY QH+E Q +W+ KKH +E PTDAFGDI F L +K KY+R+S
Sbjct: 88 VCQCGYTHEQHLEATKPHTFQGTQWDPKKHVQEMPTDAFGDIVFTGLSQKVKYVRVSQ 147

Query: 119 DTDAILLYELLTQHWHLKTPLNLVISVTGGAKNFALKPRMRKIFSR-LIYIAQSKGAWILT 177
DT + ++Y L+TQHW L PNL+ISVTGGAKNF +KPR++ IF R L+ +AQ+ GAWI+T
Sbjct: 148 DTPSSVIYHLMTQHWGLDVPNLLISVTGGAKNFNMKPRLKSIFRRGLVKVAQTGAWIIT 207

Query: 178 GCTHYGLMKYIGEVRDNTISRSEEN-IVAIGIAAWGMVSNRDTLIRNCDAEGYFLAQY 236
GD+H G+MK +GE VRD ++S S +E ++ IG+A WG V R+ LI G F A+Y
Sbjct: 208 GGSHTGVMMQVGEAVRDFSLSSSYKEGELITIGVATWGTVHRREGLIH---PTGSFPAEY 264

Query: 237 LMDDFTRDFLYILDNNHLLVNDNGCHGHTVEAKLRNQLKXYISERTIQDSNYGGKIP 296
++D+ + L LD+NH+H +LVD+G HG VE LR +LEK+ISE+T + KIP
Sbjct: 265 ILDEDGQGNLTCLDSNHSFHLVDDGTGQYGVETPLRTRLEKFISEQTKERGGVAIKIP 324

Query: 297 IVCFAQGGGKETLKAINTSIKNIKPCVVVEGSGQIADVIASLVEVE-DALTSSAVKERLV 355
IVC GG TL I+ + N PCVVVEGSG++ADVIA + + +T S +++KL
Sbjct: 325 IVCVLEGGPGTLHTIDNATTNGTTPCVVVEGSGRVADVIAQVANLPVSDITISLIQOKLS 384

Query: 356 RFLPRTVSRLPEEBETESWIKWLKEILECSHLLTVIKMEEAGDEIVSNAISYALYKAFST 415
F E W K +++I+ LLTV + + G + V AI AL KA +
Sbjct: 385 VFFQEMFETFTESRIVEWTTKIQDIVRRRQLLTVFREKDGQQDQDVAILQALLKASRSQ 444

Query: 416 EQ-DKDNWNGQLKLLLEWNQDLANDEIFTNDRRWEKSKPRLRDTIIQVTWLENGRIKVE 474
+ +NW+ QLK L + WN++D+A EIF ++ +W
Sbjct: 445 DHFGBENWDHQLKLAVAWNRVDIARSEIFMDEWQW----- 479

Query: 475 SKDVTGDKASSHMLVVVLSADLQEVMTALIKDRPKFVRLFLENGLNLRKFLTHDVLTEL 534
K +DL M ALI ++P+V+LFLENG+ L++F+T D L L
Sbjct: 480 -----KPSDLHPTMTAALISNKPEFVKLFLENGVQLKEFVTWDTLLYL 522

Query: 535 FSN-HFSTLVYRNLO-----IAKNSYNDALLTFVWKLIVANFRRGRKEDRN 579
+ N S L + LQ A + + +L+ +F + R+
Sbjct: 523 YENLDPSCLPHSKLQKVLVEDPERPACAPAPRLQMHVAVQLRELLGDFTQPLYFRPRH 582

Query: 580 GR-----DEMDELHDVS-----PITRHLQALFIWAILQNKKELSKVIW 619
+ + + VS T P++ L IWAI+QN++EL+ +IW
Sbjct: 583 NDRRLRLLLPVPHVKLVQGVSLRSYKRSRGHVTFTMDPIRDLLIWAIVQNRRELAGIIV 642

Query: 620 EQTRGCTLAALGASKLLKTLAKVKNDAAGSESELANEYETRAVELFTECYSSDEDLAE 679
Q++ C AAL SK+LK L+K + D +++ E LA EYE RA+ +FTECY DE+ A+
Sbjct: 643 AQSQDCIAAALACSKILKELSKBEEDTSSEEMLALABEYEHRAIGVPTCYRKDEERAQ 702

Query: 680 QLLVYSCEANGGSGNCLLAVEATDQHFIAQPGVQ 713
+LL EAWG + CL+LA+EA D F++ G+Q
Sbjct: 703 KLLTRVSEAWGKTTCLQLALEAKDMKFVSHGGIQ 736

FIGURE 4A

Score = 65.6 bits (157), Expect = 2e-10
Identities = 31/57 (54%), Positives = 40/57 (69%)

Query: 38 APFTSPFVVF SWNVVFI AFLLLFAYVLLMDFHSVPHPELVLYSLVFLFCDEVRO 94
AFT+F VVF N++ Y AFL LFAYVL++DF VP E +Y +F L C+E+RQ
Sbjct: 790 APFTAPVVVFHLNLSYFAFLCLFAYVLMVDFQPVPSWCECATYLNLFSLVCEEMRQ 846

FIGURE 4B

Score = 163 bits (409), Expect = 4e-39
 Identities = 90/227 (39%), Positives = 129/227 (56%), Gaps = 43/227 (18%)

Query: 144 YFTDLWNVMDTLGLFYFIAGIVFRLHSSNKSSLYSGRVIFCLDYIIFTLRLLIHIFTVSRN 203
 YF+D WN +D + F+AG+ RL + +LY GRVI LD+I+F LRL+HIFT+S+
 Subject: 863 YFSDFWNKLDVGAILLFVAGLTCLRLIPA---TLYPGRVILSLDFILFCLRLMHIFTISK 919

Query: 204 LGPKIIMLQRMSTSIEMXXXXXXIPTLRFFFEFVVLIOISISGTSSHEVMLS DRCVLLPVPL 263
 LGPKII++RM + + FF F++ + +E
 Subject: 920 LGPKIIIVKRM-----MKDVFFFLFLLAVWVVS----- 947

Query: 264 CGVDGGLCVARQGILRQNEQRWRWIFRSVIYEPYLA MFGQVPSDVGTTDFAHCTFTGN 323
 VA+Q IL NE+R W+FR +Y YL +FGQ+P +DG ++ HC+ G
 Subject: 948 -----FGVAKQAILIHNERVDWLFRCVAVHSYLTIFGQIPGYIDGVNFENPEHCSPNGT 1001

Query: 324 ES-KPLCVELD-EHNLPRFPENITIPLVCTYMLSTNILLVNLLVAMF 368
 + KP C E D P FPEW+T+ L+C+Y+L TNILL+NLL+AMF
 Subject: 1002 DPKKPKCPESDATQQRPAFFEWLTVLLCLYLLFTNILLNLLIAMF 1048

Score = 48.0 bits (112), Expect = 3e-04
 Identities = 20/45 (44%), Positives = 30/45 (66%)

Query: 475 YTVGTVQENNDQVWKFQRYFLVQVEYCSRLNIPFFPFVFAFYFYMVV 519
 YT VQE+ DQ+WKFQR+ L++EY R P PFI+ ++ + +
 Subject: 1050 YTFQVQVEHTDQIWKFQRHDLIEEYHGRPAAPPPFILLSHLQLFI 1094

FIGURE 4C

CAGGGGAGGGCTGTGCGCGTCCCATGCTTGCAAGGATGCTGACGATGCCCTTATCTCTGGGTCCAGGAAGAAACCTGTC
GACAAGCACAGAAGCTGCTTTGGTACTATGTGGCGTTCTTCACCTCCCCCTTCGTGGTCTTCTCCTGGAATGTGGTCT
TCTACATCGCCTTCCTCCTGCTGTTGCCTACGTGCTGCTCATGGATTTCCATTGGGTGCCACACCCCCCGAGCTGGT
CCTGTACTCGCTGGTCTTTGTCCTCTTCTGTGATGAAGTGAGACAG

FIGURE 5B

ATGGAGCAGGGGGTGGCGCTCGTGGAGGAGGCTCGGGCAGCACAGGAGCCCACTGAGGGGGTGGGAGGCTCAGGCATGG
 TGGGCTGCAGGTCCCGAGCCCTGCCCCACGGGAAGGCAGCTACGGCCCCCGGGTTCCCGCTCAGGCCACTCCTTCCA
 CACTTCCCTGCAAGCTGAGGGGTGCCAGCTCTGGCCTTGGCCAGCCAGAAAGGGGCTCCACAGTGCAGCGGTGGGCTG
 AAGGGCTCCTCAAGTGCCGCCAAAGTGGGAGCCAGGCAGAGGAGGTGCCGAGAGCAAGCGAGGGGCTGTGAGGACTGCC
 ACCACGCTGTCACTCTCAGAAGCGTAAGGGACTGGCTGATGTCTTATCACGGACTGGGAACAACCTGGGACAGTGTCTG
 CCCCACAACTGGGTGGTACGTAATGGGGTGAATTATTTTACTGACCTGTGAATGTGATGGACACGCTGGGGCTTTT
 TACTTCATAGCAGGAATTGTATTTTCGGCTCCACTCTTCTAATAAAAGCTCTTTGTATTCTGGACGAGTCATTTTCTGTC
 TGGACTACATTATTTTCACTCTAAGATTGATCCACATTTTACTGTAAGCAGAACTTAGGACCCCAAGATTATAATGCT
 GCAGAGGATGACGAGCATTGAGATGAGCTCATCTGGAAGCTCCATTCCAACACTGAGGTTCTTTGAGTTTGTGGTTTTA
 ATTCAAAGCATTTCTGGGACATCCAGTCATCATGAAGTCATGCTATCTGATCGATGTGTTCTTCTTCTCTCTCTTT
 CCGGTGTGGATGGTGGCCTTTGCGTGGCCAGGCAAGGGATCCTTAGGCAGAATGAGCAGCGCTGGAGGTGGATATTCG
 TTCGGTCTATCTACGAGCCCTACCTGGCCATGTTCCGGCCAGGTGCCAGTGACGTGGATGGTACCACGTATGACTTTGCC
 CACTGCACCTTCACTGGGAATGAGTCCAAGCCACTGTGTGTGGAGCTGGATGAGCACAACCTGCCCCGGTTCCCCGAGT
 GGATCACCATCCCCCTGGTGTGCATCTACATGTTATCCACCAACATCCTGCTGGTCAACCTGCTGGTCCGCATGTTTGG
 GTGTGTAGCCGCTGGCCTAGTTCAAGTTCTTGACTTTGGGACAGAAAATAATTTGAAAGTGAGTCAAAAGCAAAAGCAA
 GCAAGAGAGTTCACTGCAAAGCCAAATACACTCTAGCAGCCGCTGGTTTCAGGAGATGGACCTCAGCTGTCACTGCAT
 GTCTCCAGCCAGCTAGGTGTTTGGCAGGGACAGGACGCCAAGGGCACAAGATATCGCTGGAGATGCACAAAGGGAAAAAT
 TGCAGAAATCTCTCAGGGACAACACCAGATGGCCACTGGTTGTCAAGGAGACTTAAAGAACCATCTCAGATGGGGCGGC
 TACACGCTGGGCACCGTCCAGGAGAACAATGACCAGGTCTGGAAGTTCCAGAGGTACTTCTGGTGCAGGAGTACTGCA
 GCCCGCTCAATATCCCTTCCCTTTCATCGTCTTCGCTTACTTCTACATGGTGGTGAAGAAGTGCTTCAAGTGTGCTG
 CAACGAGAAAAACATGGAGTCTTCTGTCTGCTCTGTGGAGGCAGGTGAAGATGCTTACAATTATAGGGAACATAAGGAA
 CGCTCAAAACAGCTTTTGGGAGCCAGTGTGCCTTGATGCTAGTCTTTGCTGCCACTCTGATTGCTTGCCTGTTTTATT
 TGGAGGCCATTGGAAATGCGTGA

FIGURE 5C

1	11	21	31	41	51	
1	MASWCLITAQ	VWVKMGDVV	GSRSFQQHKR	STGTPQGLPV	PISEGSMSKF	LPVHTIVLIR 60
61	ENVCKCGYAQ	SOHMEGTQIN	QSEKWNYYKKH	TKEFPTDAFG	DIQFETLGKK	GKYIRLSCDT 120
121	DABILYELLT	QHWHLKTPNL	VISVTGGAKN	FALKPRMRKI	FSRLIYIAQS	KGAWILTGGT 180
181	HYGLMKYIGE	VVRDNTISRS	SEENIVAIGI	AAWGMVSNRD	TLIRNCDAEG	YFLAQYLMDD 240
241	FTRDPLYILD	NNHTHLLLVD	NGCHGHPTVE	AKLRNQLKY	ISERTIQDSN	YGGKIPVCF 300
301	AQGOGKETLK	AINTSIKNKI	PCVVVEGEGQ	IADVIASLVE	VEDALTSSAV	KEKLVRFLLR 360
361	TVSRLPESET	ESWIKWLKEI	LECSHLLTVI	KMEAGDEIV	SNAISYALYK	AFSTSEQDKD 420
421	NWNGQLKLLI	EWNQDLAND	BIFTNDRWE	KSKPRLRDTI	IQVTWLENGR	IKVESKDVTD 480
481	GKASSHMLVV	LKSADLQEVN	FTALIKDRPK	FVRLFLENGL	NLRKFLTHDV	LTELFSDHFS 540
541	TLVYKRLQIA	KNSYNDALLT	FVWKLVAEFR	RGPRKEDRNG	RDEMDIELHD	VSPITRHFLO 600
601	ALFIWAILQN	KKELSKVIWE	QTRGCTLAAL	GASKLLKTLA	KVKNDINAAG	ESSELANEYE 660
661	TRAVRLFTEC	YSSDEDLAEQ	LLVYSCEAWG	GSNCLELAVE	ATDQHFIAQP	GVQ

FIGURE 6A

1	11	21	31	41	51	
1	RGGLCPSHAC	KDADDALISG	SRKKPVDKHK	KLLWYYVAFF	<u>TSPFVVFSWN</u>	<u>VVFYIAFLLL</u> 60
61	<u>FAYVLLMDPH</u>	<u>SVPHPFELVL</u>	YSLVFFVLFCD	EVRQ		

FIGURE 6B

1	11	21	31	41	51		
1	MEQGVAVVEE	ARAAQEPTTEG	VGGSGMVGCR	SRALPHGKAA	TARPGSRSRH	SFHTSLQAEG	60
61	ASSOLGQPRK	GLPQCSGGLK	GSSSAKVGA	QAEVFRASE	GCEDCQHAVT	SQKRKGLADV	120
121	LSRTGNWDS	VCPTSGWYVN	GVNYFTDLWN	<u>VMOTLGLFYF</u>	<u>IAGIVERLHS</u>	SNKSSLYSGR	180
181	<u>VIFCLDYIIF</u>	<u>TLRLIHIFTV</u>	SRNLGPKIIM	LQMTSIEMS	SGSSSIPTLE	FFEFVLIQS	240
241	ISGTSSHHEV	<u>MLSDRCVLLP</u>	<u>VLPCGVDGGL</u>	<u>CVARQGILRQ</u>	NEQRWRWIFR	SVIYEPYLAM	300
301	FGQVPSDVDG	TTYDFAHCTF	TGNESKPLCV	ELDEHNLPRF	<u>PEWITIPLVC</u>	<u>IYMLSTNILL</u>	360
361	<u>VNLIVAMFGC</u>	<u>VAGGLVQVLD</u>	FGTENNLRVS	QKQKQARELT	AKPKYTLAAA	GFRRWTSAVT	420
421	ACIQPARCLP	GTGRQGHKIS	LEMHKGKIAE	FSQGQHQMAT	GCQGDFKNHL	RWGGYTVGTV	480
481	QENNDQVWKF	QRYFLVQEXC	<u>SRLNIPFFFI</u>	<u>VFAYFYMVVK</u>	KCFKCCCKEK	NMESSVCSVE	540
541	AGEDAYNYRE	HKEGSKRLFG	<u>SQCAIMLVFA</u>	<u>ATLIRCLFYL</u>	<u>EGIGNA</u>		

FIGURE 6C

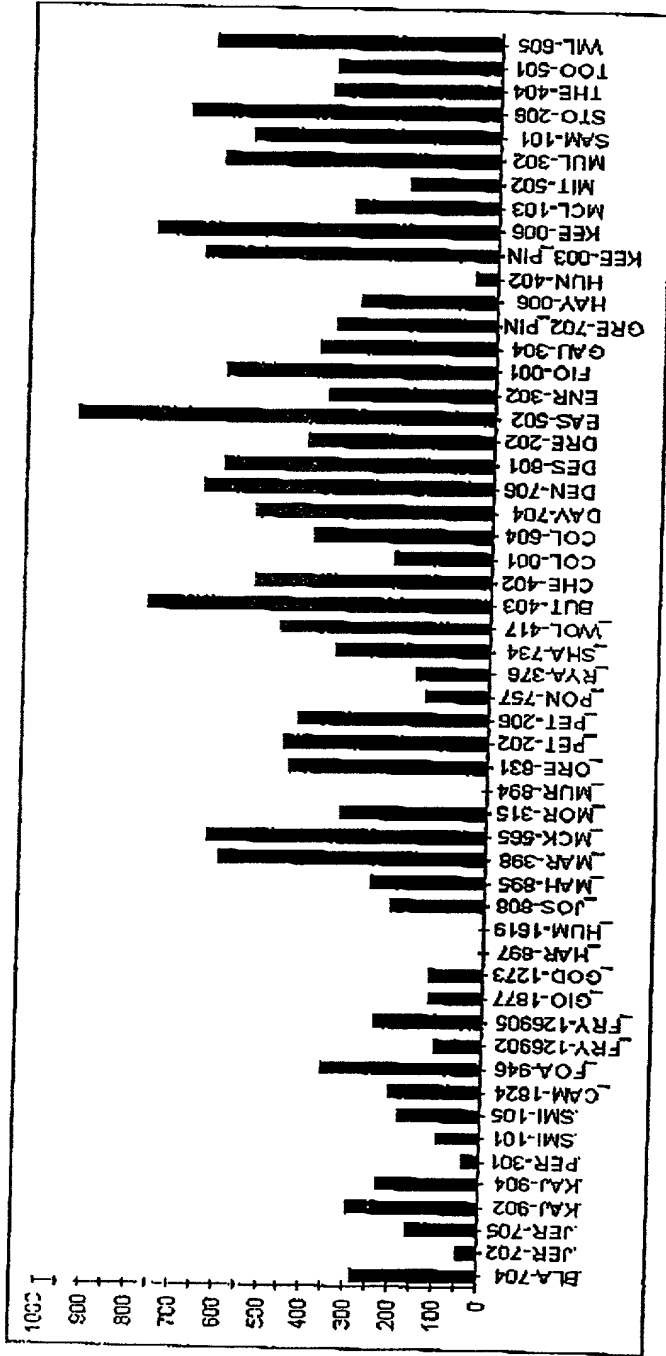


FIGURE 3A

10058543 012402

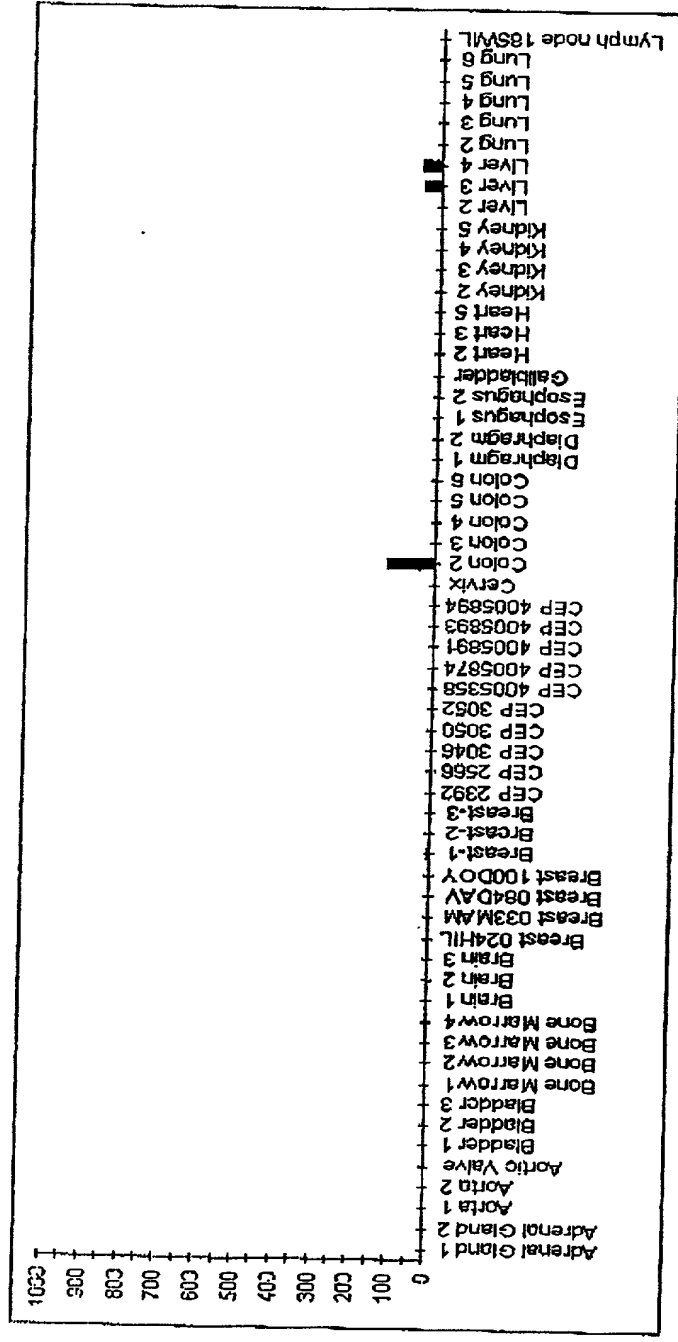


FIGURE 3B

